Evaluation of ONT MinION accuracy in interrogating mosquito pools from surveillance systems

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INTRODUCTION

Vector-borne diseases are responsible for 17% of all infectious diseases and account for over 700 000 deaths annually, mainly in Sub-Saharan Africa[1]. Malaria and Dengue are the deadliest and most prevalent, respectively, of all. Vector surveillance is crucial for monitoring vector control programmes which aim to tackle these diseases[2].

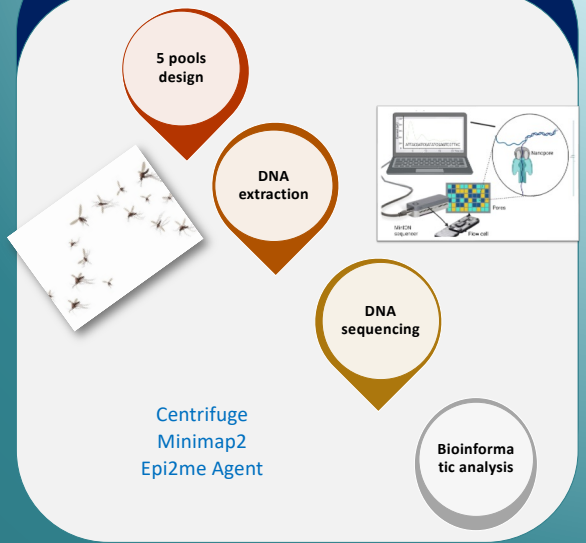
Surveillance provides critical information for decision-making policies, ensuring vector control programmes are and remain effective. The current tests used for mosquito surveillance are often of difficult implementation, with high error and do not consider new circulating vectors and pathogens[3].

Genomics can overcame this by allowing the study of genetic material, thus informing on population compositions, insecticide resistance origin and behaviour. Its costs and training requirements have hampered its use at a regional levels leading to gaps between policy-making and field/regional program requirements. The direct, portable, USB MinION sequencer from ONT with its low operational costs could change this by allowing routine surveillance studies directly in regional settings.

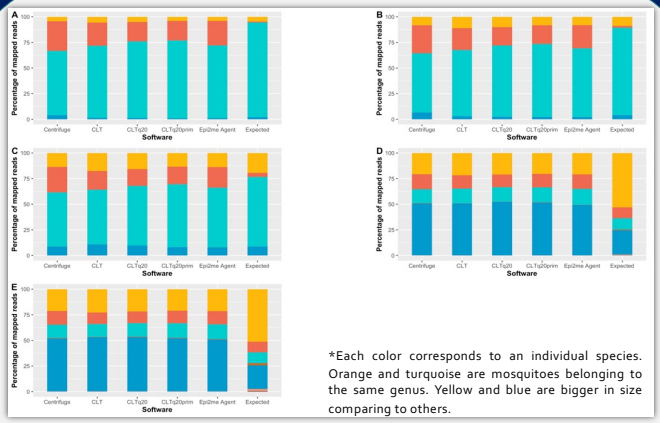
RESEARCH AIMS

Test the efficiency of MinION sequencer in interrogating mosquito pools with minimal bioinformatic analysis requirements.

METHODOLOGY



RESULTS



*Each color corresponds to an individual species. Orange and turquoise are mosquitoes belonging to the same genus. Yellow and blue are bigger in size comparing to others.

- Difficulty assigning reads between same genus.
- Different proportions than expected when in same quantity

Model fit (vs expected)	Spearman Rho	*p*-value	*p*-value adjusted (Bonferroni)
Centrifuge	0.57	0.0025	0.0125
CLT	0.63	0.00059	0.002950
CLTq20	0.71	0.000051	0.000255
CLTq20prim	0.72	0.000032	0.000160
Epi2me Agent	0.67	0.00019	0.000950

DISCUSSION/CONCLUSION

Whole genome sequencing appears to result in difficulties assigning reads between vectors belonging to the same species. Mosquito weight and size might have influence in the distribution of the number of reads. When using WGS, correction of reads is important, similarly to what performed in RNA-sequencing analysis[4]. A targeted approach should be tested for mosquito/pathogen identification and reduction in costs[5].

FUTURE RESEARCH

An *in-silico* approach is being conducted with the WGS data to detect specific barcoding genes. Another set of pools were prepared by amplifying specific genes before sequencing. This pipeline will be tested in traps from endemic countries.

REFERENCES

1. Vector-borne diseases [Internet]. [cited 2023 Apr 3]. Available from: https://www.who.int/news-room/fact-sheets/detail/vector-borne-diseases
2. Kramer RA, Dickinson KL, Anderson RM, Fowler VG, Miranda ML, Mutero CM, et al. Using Decision Analysis to Improve Malaria Control Policy Making. Health Policy [Internet]. 2009 Oct [cited 2023 Apr 3];92(0):133. Available from: /pmc/articles/PMC3645449/
3. Nsanzabana C. Strengthening Surveillance Systems for Malaria Elimination by Integrating Molecular and Genomic Data. Trop Med Infect Dis [Internet]. 2019 [cited 2023 Apr 3];4(4). Available from: /pmc/articles/PMC6958499/
4. Campos M, Phelan J, Spadar A, Collins E, Gonçalves A, Pelloquin B, et al. High-throughput barcoding method for the genetic surveillance of insecticide resistance and species identification in Anopheles gambiae complex malaria vectors. Sci Rep [Internet]. 2022 Dec 1 [cited 2023 Apr 3];12(1):13893. Available from: /pmc/articles/PMC9381500/
5.Conesa A, Madrigal P, Tarazona S, Gomez-Cabrero D, Cervera A, McPherson A, et al. A survey of best practices for RNA-seq data analysis. Genome Biology 2016 17:1 [Internet]. 2016 Jan 26 [cited 2023 Apr 3];17(1):1–19. Available from: https://genomebiology.biomedcentral.com/articles/10.1186/s13059-016-0881-8